ES prok gamma Differential expression HvN_no_outs

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ID	Image	logFC	p-Value
k141_613170_31_Forms_part_of_the_polypeptide_exit_	6	-3.19	0.000473 (
k141_27241_1_NQR_complex_catalyzes_the_reduction_o	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_27241_1_NQR_compl	-2.61	0.000954 (
k141_470066_2_Belongs_to_the_TPP_enzyme_family	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_470066_2_Belongs_to	-2.55	0.000387 (
k141_2524_2_Participates_in_both_transcription_ter	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_2524_2_Participates_i	-2.51	0.002170 (
k141_1203270_2_Carrier_of_the_growing_fatty_acid_c	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_1203270_2_Carrier_of	-2.31	0.002640 (
k141_9480_17_Catalyzes_the_anti-1_4-elimination_of	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_9480_17_Catalyzes_t	-2.17	0.002210 (
k141_36540_1_membrane_proteinhomolog_of_Drosophi	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_36540_1_membrane	-2.07	0.001410 (
k141_626670_10_Bacterial_regulatory_helix-turn-hel	60	-2.04	0.003640 (
k141_629515_3_PFAM_Cytochrome_cclass_I	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_629515_3_PFAM_Cyt	-2.02	0.000985 (
k141_648253_12_D-isomer_specific_2-hydroxyacid_deh	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_648253_12_D-isomer	-2.01	0.001420 (
k141_743581_7_Catalyzes_the_phosphorylation_of_the	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_743581_7_Catalyzes	-2.01	0.002870 (
k141_995324_1_TIGRFAM_glutamine_synthetasetype_I	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_995324_1_TIGRFAM	-1.98	0.000570 (
k141_1022530_1_Belongs_to_the_CDP-alcohol_phosphat	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_1022530_1_Belongs_t	-1.97	0.002850 (
k141_237243_12_COG0659_Sulfate_permease_and_relate	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_237243_12_COG0659	-1.95	0.001440 (
k141_1008173_3_Histidine_kinase	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_1008173_3_Histidine	-1.92	0.000822 (
k141_1203270_1_Catalyzes_the_condensation_reaction	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_1203270_1_Catalyzes	-1.92	0.003270 (
k141_212078_2_DsrE_DsrF-like_family	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_212078_2_DsrE_DsrF	-1.87	0.002890 (
k141_744041_3_PFAM_Rhodanese-like	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_744041_3_PFAM_Rho	-1.86	0.003140 (
k141_748209_3_DoxX_family	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_748209_3_DoxX_famil	-1.85	0.001150 (
k141_1141696_11_PFAM_ErfK_YbiS_YcfS_YnhG_family_pr	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_1141696_11_PFAM_E	-1.80	0.001730 (
k141_561840_2_Required_to_facilitate_the_formation	6-0 3 366 (figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_561840_2_Required_t	-1.77	0.001660 (
k141_60267_2_Catalyzes_the_hydrolysis_of_inorganic	•	-1.77	0.003360 (
k141_60267_4_PFAM_Hydantoinase_B_oxoprolinase	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	-1.73	0.002310 (
k141_392000_2_Thiol-specific_peroxidase_that_catal	6	-1.69	0.003420 (
k141_965211_7_COG0616_Periplasmic_serine_proteases	•• Oloo Oloo Oloo Oloo Oloo Oloo Oloo Olo	-1.69	0.001890 (
k141_57623_2_Belongs_to_the_bacterial_solute-bindi	o o o o o o o o o o o o o o o o o o o	-1.67	0.002770 (

		From	From to	1
		to	10	
ID	Image	logFC	p-Value	í
k141_744041_4_Belongs_to_the_peptidase_S41A_family	6(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_744041_4_Belongs_to	-1.64	0.002290	(
k141_613170_12_The_central_subunit_of_the_protein_	o ♦©	-1.54	0.003460	(
k141_257411_6_reductasedissimilatory-type_beta_s	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_257411_6_reductase	-1.39	0.003080	(
k141_376279_3_Type_I_restriction-modification_syst	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_376279_3_Type_I_res	1.65	0.001180	(
k141_699512_3_signal_sequence_binding	6	2.47	0.000179	(
k141_669450_29_flavin_adenine_dinucleotide_binding	(figuresES_prok_gamma_RNAseq_analysis_with_DESeq2_long_names_HvN_no_outs/boxplot.k141_669450_29_flavin_ade	2.60	0.000984	(

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